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254: gb_est185:*
255: gb_est186:*
256: gb_est187:*
257: gb_est188:*
258: gb_est189:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT	2	
LOCUS	BF726094	429 bp mRNA
DEFINITION	bx23h10.y1 Human iris cDNA (un-normalized, unamplified): Bx Homo sapiens cDNA clone Bx23h10 5', mRNA sequence.	05-JAN-2001
ACCESSION	BF726094	
VERSION	BF726094.1	GI:12042005
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 429)	
TITLE	Mistow,G.J., Bernstein,S., Behl,A. and Smith,D.	
JOURNAL	NEIBANK: EST analysis and bioinformatics for ocular genomics invest. Ophthalmol. Vis. Sci. 41 (2000) in press	
COMMENT	Contract: Mistow G Section on Molecular Structure and Function National Eye Institute 6/331, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 23 row: h column: 10 Seq primer: M13Rp1 reverse primer (AB1). Location/Qualifiers 1..429 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="bx23h10" /clone_lib="Human Iris cDNA (un-normalized, unamplified): Bx" /tissue_type="Iris" /dev_stage="Adult" /lab_host="EMDH10B" /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the Superscript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetechn.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTCTGATGCGCAGCGGCCGCC(7)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoRV sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."	
FEATURES	source	
BASE COUNT	107 a 129 c 130 g 63 t	
ORIGIN		
Query Match	7.0%; Score 429; DB 166; Length 429;	
Best Local Similarity	100.0%; Prid. No. 1.7e-65;	
Matches 429; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Db	1 CAGCGTCACACTGCTGCTTGCGCTTCGCTGCTGATGTGGGATGTGGGGCCAGACAGCTC	60
5443	agctcaggaaagccaatataccagagtcgcagatgcagatacaccctcaagtctggcagc	5502
61	AGCTCAGGAAGGCCAATATACACAGAGTGGCCATGCAATATACCTTTCAGTGTGGCCAGT	120
5503	ccaatgaatccagcttgcgcagagcagagccagccatgctcagtcatacctaactacaga	5562
121	CCAATGATTCAGCTGCCAGACAGACGACGAGCCATGTCATGCATTAACCTTAACAGA	180
5563	gagacagcagcaccacacagcttgaacctggagggcaccacaaagctcgaactcagctccctg	5622

QY	1321	accgagagctactgtgaacctctgcctcccaaggttaagaacattctctgtctcagactcc	1380				
Db	293	ATCTCAGCTCAGCTGCAACCTCTGCTCCCGGCTCAAGGAGATTCTCTCTCAGCTCC	352				
QY	5623	agagcctccctcccaacaaattgaactcttgacccaagctctcccaagcccaagaga	5662				
Db	241	AGAGCTCTCTCCACCAATTGACCTTGGACCAAGCTGTCAGGCCCCAGAGACCCAGAGG	300				
QY	5683	gagctcagaagagagcctgagcacccttgagagcgagagcgagaccagcttgaaaccca	5742				
Db	301	GGCTGCAGAGAGGAGCTGGGACACCTTAGGCGGGAGCGGACACACTGTGAAACCAACCA	360				
QY	5743	gagagcttgagagactgctctacagcaacctctccgagacaagtcaagctctgagagaaga	5802				
Db	361	GAGAGTTGGAGACTGCTACAGCAACCTCCTCCGAGACAAGTCACTGTGAGAGAAAGA	420				
QY	5803	agaagcgac	5811				
Db	421	AGAGCGAC	429				
RESULT	3	AQ057239	660 bp	DNA	GSS	30-JUL-1998	
LOCUS		CIT-HSP-2340D14.TF	CIT-HSP	Homo sapiens	genomic clone	Z340D14	DNA
DEFINITION			sequence.				
ACCESSION		AQ057239					
VERSION		AQ057239.1	GI:3353765				
KEYWORDS		GSS.					
SOURCE		human.					
ORGANISM		Homo sapiens					
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS		Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M., and Venter,J.C.					
TITLE		Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)					
JOURNAL		Unpublished (1998)					
COMMENT		Other GSS: CIT-HSP-2340D14.TF					
		Contact: Mark Adams					
		Department of Eukaryotic Genomics					
		The Institute for Genomic Research					
		9712 Medical Center Dr., Rockville, MD 20850, USA					
		Tel: 301 838 0200					
		Fax: 301 838 0208					
		Email: mdadams@tigr.org					
		Clones are available from Research Genetics (info@resgen.com). BAC					
		end search page:					
		http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.					
		Seq primer: M13 Reverse					
		Class: BAC ends.					
FEATURES		Location/Qualifiers					
Source		1..660					
		/organism="Homo sapiens"					
		/db_xref="taxon:9606"					
		/clone="Z340D14"					
		/clone_lib="CIT-HSP"					
		/sex="Male"					
		/cell-type="Sperm"					
		/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"					
BASE COUNT		116 a	188 c	150 g	206 t		
ORIGIN							
Query Match		2.9%;	Score 180.8;	DB 223;	Length 660;		
Best Local Similarity		86.0%;	Pred. No. 5.9e-22;				
Matches 215;		Conservative 0;	Mismatches 27;	Indels 8;	Gaps 1		

OY	1381	cgagtagctggagactacagggc-----caagcccggcctaatctttgcatgtagta	1432
DB	353	CAAGTACTGGGATTACAGCGCGACACACCACCACCCCGGCTAATTTTGTATTTTAAGTA	412
OY	1433	gagatgggggttccacatatatagccggcgtgctctgaactccgacctaagaatga	1492
DB	413	GAGATGGGGGTTTCAACAGATGTGGCCAGGCTGGTCTGCAACTCCGTGACCTCAGGAGATCCA	472
OY	1493	cccaactcagcctccctaaagtgtcgtgggattacagcatgatcaccgcccggccaagg	1552
DB	473	CCCACTCTGCTCTCCCAAAAGTGGGAGATTACAGAGCCTGGGCGCACTGCGCCAGCCTAAT	532
OY	1553	gtcagtgctt 1562	
DB	533	TTTTGTATT 542	
RESULT	4		
LOCUS	A0379787/c		
DEFINITION	A0379787	539 bp	DNA
ACCESSION	A0379787		
VERSION	A0379787.1	GI:4350810	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
	1 (bases 1 to 539)		
	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter		
	,J.C.		
TITLE	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready		
JOURNAL	Map Building		
COMMENT	Unpublished (1997)		
	Contact: Shaying Zhao, William Nierman, Mark Adams		
	Department of Eukaryotic Genomics		
	The Institute for Genomic Research		
	9712 Medical Center Dr., Rockville, MD 20850		
	Tel: 301 838 0200		
	Fax: 301 838 0208		
	Email: hbe@ligr.org		
	Clones are derived from the human BAC library RPCI-11. For BAC		
	library availability, please contact Plier de Jong		
	(plierdejong.med.bufileo.edu). Clones may be purchased from		
	BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from		
	Research Genetics (info@resgen.com). BAC end search page:		
	http://www.ligr.org/tldb/humgen/bac_end_search/bac_end_search.html		
	Seq primer: SP6		
	Class: BAC ends.		
FEATURES			
Source	Location/Qualifiers		
	1..539		
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	/db_xref="GDB:7558034"		
	/db_xref="taxon:9606"		
	/clone="RPCI-11-152C3"		
	/clone.lib="RPCI-11"		
	/sex="Male"		
	/cell_type="lymphocytes"		
	/note="vector: pBACe3.6; site_1: EcoRI; site_2: EcoRI;		
	RPCI11 Human Male BAC Library"		
BASE COUNT	187 a 112 c 123 g 116 t	1	others
ORIGIN			
Query Match	2.9%	Score 179.8;	DB 227; Length 539;
Best Local Similarity	76.8%	Pred. No. 9e-22;	
Matches 235; Conservative	0;	Mismatches 63;	Indels 8; Gaps
OY	1280	aggaggaagagctgtgtctacactaccgtatgacctacactagctcactgcacac	1339
DB	327	AGAGTCTGCTGTGCACACAGGTGGAGTTCAGTGGCGGGGATCTGGGCTACATGCACAC	268

OY	1340	tcgcctcccaaggtcgaagaattctctcgtctccaaacctcccggcgtagtctggaactaacg	1399
Db	267	TTCTGCTCCCGGGTTCAGCAATTTCCTCCTCACGCCCTCCGAGTAGCTGGACCACAG	208
OY	1400	gc-----gcacgcccgctaatttttgatctgttaagaatgagggttccaata	1451
Db	207	GCAATGTGCACACATACCCCGGCTAATTTTTTGTTATTTTACTAGAAACGGSGTTTCACATG	148
OY	1452	ttaagccgcgctgctctgaactccctcgaactcaagtgatccaccacctaagcctctaa	1511
Db	147	TTGGCCAGAGCTGCTGTAACCTCCTGACCTCAGAGTGATCACACAGCCTTGCCCTCTAAA	88
OY	1512	gtgctctggaatcaagcgcatgaagtccacgcgcgcgcgcgaaggtcagtgctttaataagaa	1571
Db	87	GTGCTGGGATTTACAGAGTGATGATCACACGCCCGGCTCAATATCCCTTTTTCACAGCTGA	28
OY	1572	tcaact 1577	
Db	27	TGAATT 22	
RESULT	5		
LOCUS	AZ520729	613 bp DNA	GSS 16-OCT-2000
DEFINITION	RPC11-11-7965.TJ.D RPC11-11 Homo sapiens genomic clone RPC11-11-7965,		
ACCESSION	AZ520729	DNA sequence.	
VERSION	AZ520729		
KEYWORDS	AZ520729.1 GI:108333239		
SOURCE	GSS.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 613) Zhao,S., Adams,M.D., Niernan,W., Malek,J., de Jong,P. and Venter ,J.C. BAC end sequences of library RPC11-11 Unpublished (1997) Other_GSSs: RPC11-11-7965..TJ RPC11-11-7965.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the human BAC library RPC11-11. For BAC library availability, please contact Pieter de Jong (pietere@jeng.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering/) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hunguen/bac_end_search/bac_end_search.html This BAC end was generated during the Rad process and may have higher chance of clone tracking errors. Seq primer: Sp6 Class: BAC ends.		
FEATURES			
SOURCE	Location/Qualifiers		
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	/db_xref="GB:"7530100"		
	/db_xref="taxon:9606"		
	/clone="RPC11-11-7965"		
	/clone_1ib="RPC11-11"		
	/sex="Male"		
	/cell_type="Lymphocytes"		
	/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;		
	RPC11 Human Male BAC Library"		
BASE COUNT	153 a 134 c 141 g 185 t		
ORIGIN			
Query Match	2.9%	Score 179;	DB 245; Length 613;
Best Local Similarity	76.4%	Pred No. 1.2e-21;	

Matches	236:	Conservative	0:	Mismatches	65:	Indels	8:	Gaps	1
OY	1280	agggtgagagggtctgtgtgtcttacacttaacctgtatgctctacacctgagctacatgcaacc							1339
Db	118	AGAGCTCTTGCTCTTGCGCCACAGCTGAGATACAGAGGTGCGATGTCACCTCACTCGAACCC							177
OY	1340	ctgtgcttcaccaggtctcaagcaattctcctgtcttgagccctccggcgtaagcttgagactaacg							1399
Db	178	TCTGACTCTCTGGGTTCAMACCAATTCCTCGTGTTAGCCCCCGAGTAGCTGGGATTTACAG							237
OY	1400	gcg-----caagcccgccgaactcttctgtatctgtatgtagagagaatgaggtcttcaccata							1451
Db	238	GTGGCTGGCCACCATTCGCTACGTAATTTGTGTATTTTACAGACAGATGGGGTTTCACACATA							297
OY	1452	ctagcccgagctgtgctctgaaactctgaaactcaagtcagatccaccacactcaagcctctctaaa							1511
Db	298	TTGGTCAAGGCTGTGTGGAACTCGACCTCAGGTGATGCACACCGCGTCCAGCTCCGAAA							357
OY	1512	gtgctgaggaattacagcaatgagtcaaccgagcccgcccaaggttcagtgcttctaataagaa							1571
Db	358	GTGGCTGGGATTTACAGAGCGTGAACACCGTGCCTGGTGTCCAGGGGTGATGTTTTTATAGGAA							417
OY	1572	taacttgaa	1580						
Db	418	TAAATTCGA	426						

RESULT	6
A0636457/c	
LOCUS	
DEFINITION	A0636457 645 bp DNA
DESCRIPTION	RPCI-11-465121.JU RPCI-11 Homo sapiens genomic clone RPCI-11-465121 , DNA sequence.

SOURCE ORGANISM

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 645)

Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter

TITLE	Use of BAC End Sequences from Library RCI-11 for Sequence-Ready Map Building
JOURNAL	Unpublished (1997)
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet1@ig.org
Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/>) or from Research Genet cs (<http://inforesgen.com>). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Sfo
Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .645

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/organism="Homo sapiens"
/db_xref="CDB:7678388"
/db_xref="taxon:9606"
/clone="RPCT-11-465121"
/clone_1lb="RPCT-11"
/sex="Male"
/cell_type="Lymphocytes"
/notes="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI"
RCC11 Human Male BAC Library"
BASE COUNT
214 a 118 c 139 g 174 t

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Query Match	2.9%	Score 179;	DB 231;	Length 645;
Best Local Similarity	88.2%;	Pred. No. 1.2e-21;		
Matches 209; Conservative	0;	Mismatches 20;	Indels 8;	Gaps 1;

QY 1382 gcgtagctggaactacagcg-----caagcccgctaatttctglatgtatag 14333

Db 188 GAGTAGCTGGGATTTACAGCGGCTGTGCACACAGCCACGACTATTTTGGATTTATAG 129

QY 1434 agatagggttcaacatattagccggctcgtgcttgaactctctgaccctcagtgatcac 14933

Db 128 AGAAGGATTTACACAGTGTGGCCAGGCGTGTCTCGACTCTGCACCTCAAGTATGTGC 69

QY 1494 ccacctcagcctccataagtcgtcggatattacaggcaatgattacgcgcgcggcgcaa 1550

Db 68 CCACTCAGCGCTCCCAAGTGTGCTGGGATTTACAGGCTTGAGGCCCGCGCGCGCAA 12

RESULT	7
AO387027/c	
LOCUS	678 bp DNA
DEFINITION	GSS
	21-MAY-1999
	RPC111-153C12.TU RPC1-11 Homo sapiens genomic clone RPC1-11-153C12 DNA sequence.

ACCESSION	AQ387027	
VERSION	AQ387027.1	GI:4358050
KEYWORDS	GSS.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
1 (bases 1 to 678)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venker
J.C.

TITLE	Use of BAC End Sequences from Library RPCI-11 for Sequence-ready
JOURNAL	Map Building
COMMENT	Unpublished (1997)
Other_GSSS:	RPC11-153C12.TV

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org

Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tlgr.org/tcdb/humgen/bac_end_search/bac_end_search.html

Seq primer: Sp6
Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .678

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/db_xref="GDB:7558427"
/db_xref="taxon:9606"
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/clone_1lb="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RcCl1 Human Male BAC Library"
BASE COUNT      210 a      151 c      171 g      146 t

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Query match 2.98; Score 179; DB 227; Length 678;

Query Match	2.9%	Score 179;	DB 231;	Length 645;
Best Local Similarity	88.2%;	Pred. No. 1.2e-21;		
Matches 209; Conservative	0;	Mismatches 20;	Indels 8;	Gaps 1;

QY 1382 gcgtagctggaactacagcg-----caagcccgctaatttctglatgtatag 14333

Db 188 GAGTAGCTGGGATTTACAGCGGCTGTGCACACAGCCACGACTATTTTGGATTTATAG 129

QY 1434 agatagggtttaaacaatatagaccggtctggtcttgaactctctgaccctcagtgatcac 14933

Db 128 AGAAGGATTTACACAGTGTGGCCAGGCGTGTCTCGACTCTGCACCTCAAGTAGTATGCG 69

QY 1494 ccacctcagcctccaaagtgtctggagattacaggaatagatctacgcgcgcgcgcga 1550

Db 68 CCACTCAGCGCTCCCAAGTGTGCTGGGATTAACAGGCTTAGAGCCACCGCGCCGGCCAA 12

RESULT	7
LOCUS	AO387027/c
DEFINITION	AO387027 678 bp DNA GSS RPF11-153C12.TU RPF1-11 Homo sapiens genomic clone RPF1-11-153C12 DNA sequence.

ACCESSION	AQ387027	
VERSION	AQ387027.1	GI:4358050
KEYWORDS	GSS.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
1 (bases 1 to 678)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venker
J.C.

TITLE	Use of BAC End Sequences from Library RPCI-11 for Sequence-ready
JOURNAL	Map Building
COMMENT	Unpublished (1997)
Other_GSSS:	RPC11-153C12.TV

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetlgr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tlgr.org/tcdb/humgen/bac_end_search/bac_end_search.html

Seq primer: Sp6
Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .678

```

/organism="Homo sapiens"
/db_xref="CDB:7558427"
/db_xref="taxon:9606"
/clone="RPCI-11-153C12"
/clone_1lb="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RcCl1 Human Male BAC Library"
BASE COUNT      210 a      151 c      171 g      146 t

```

Query match 2.98; Score 179; DB 227; Length 678;

Best Local Similarity 77.4%; Pred. No. 1.2e-21;
Matches 233; Conservative 0; Mismatches 60; Indels 8; Gaps 1;

```
OY 1274 tccgagaggggtgaggtgtgtgtgtcttacaccctgtatgtcttaacccttgagctact 1333
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 364 TCAGCACAGAGCTTCTGCTGTGTGCTCAGGCTGGAGTGCAGATGCGATCTCGCTCACT 305
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1334 gcaaccctctgcctcccaaggttcaagaactctctctgtctcaagcctcccgctagctgga 1393
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 304 GCAACGCTCGGCTCCGACAGTTTCAGACATTCCTCGCTCAAGCTCCATGATGAGTGGGA 245
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1394 ctcaagagc-----gcaagcccgagctaatcttctgtatctgttagtagagatggggcttc 1445
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 244 TTACAGCACCACCCACCACCATGCCCCGCTAATTTTATTTTATTTAGATGAGGAGGTTTC 185
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1446 accatataagccgggtgtgtcttgtaacctctgtacctagctaggtgataccaccactaagct 1505
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 ACCATGTTGGCAGGCTGGTCTCGAATCTGACCTCAGGTGATCTGCGCCGCTTAGGCT 125
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1506 cctaaagtcctggggtctacaggcatgagctcaagcgcgcgcgcgcgaagggtcagtgcttaac 1565
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 124 CCCAAGGCTGTGGATTTACAGGCGTGAGCCACGCGCCGCTTATTTATTTTATTTAG 65
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1566 a 1566
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 64 A 64
```

RESULT 8
BG541228/c 887 bp mRNA EST 03-APR-2001
LOCUS 602570320F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694813 5',
DEFINITION mRNA sequence.
ACCESSION BG541228
VERSION BG541228.1 GI:13533461
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 887)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaubs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LICM1519 row: g column: 06
High quality sequence stop: 619.

FEATURES
source Location/Qualifiers

1..887
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: Lung; Vector: pPNR-LIB (Clontech); Site: 1;
Site1 (ggccgcctcgccg); Site2: Site1 (ggccatctggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATATATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGACGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC library."

BASE COUNT 260 a 215 c 236 g 176 t

ORIGIN

Query Match 2.9%; Score 178.6; DB 155; Length 887;
Best Local Similarity 77.6%; Pred. No. 1.4e-21;
Matches 232; Conservative 0; Mismatches 59; Indels 8; Gaps 1;

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OY 1281 gggtagaggtctgtgtcttacaccctgtatgtcttaacccttgagcttaaccct 1340
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 427 GAGTCTCGCTGTGTGCTGCCAGGCTGGAGGCGAGTGGCATGATCTTGCTCACTGCACAT 368
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1341 ctgcctcccaaggttcaagaactctctctgtctcaagcctcccgctagcttgagactaagg 1400
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 367 CCGGCTCCCGGCTTCCAGCAATTCCTGACCTCAGGTATCCACCCTCCAGTAGTGGGATTAACAG 308
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1401 c-----gcaagcccgagctaatcttctgtatctgttagtagagatgggggttaccatat 1452
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 307 CCTGTGCCACACGCGCCGCTAATTTTGTATTTTATTTAGAGAGAGAGGCGGCTTCTCATCT 248
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1453 tagccgcgtgtgtcttgacctctgaacctcaaggtgatccaccacttaagctcctaaag 1512
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 247 TGGCCAGGCTGGTCTTGAATCTTGACCTCAGGTATCCACCCTCGGCTCCCAAG 188
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1513 tgcctggaattacaagcatgacagtcacgcgcgcgcgcgaagggtcagtgcttaagaa 1571
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 187 TGCTGGATTTACAGGAGTGCAGCCGCCGCGGCTGGAATCAGCTTTTAACGTGAA 129
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 9
AM978041 537 bp mRNA EST 02-JUN-2000
LOCUS EST390150 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
DEFINITION AM978041
ACCESSION AM978041
VERSION AM978041.1 GI:8169303
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 537)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt,
I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeaman, T. J. and
Quackenbush, J.
TITLES Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johng@tigr.org
Plate: 387
Seq primer: Forward.

FEATURES
source Location/Qualifiers

1..537
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="MAGE resequences, MAGE"
/note="Vector: pBluescriptsKm"
BASE COUNT 119 a 157 c 141 g 118 t 2 others
ORIGIN

Query Match 2.9%; Score 178.4; DB 123; Length 537;
Best Local Similarity 77.2%; Pred. No. 1.6e-21;
Matches 233; Conservative 0; Mismatches 61; Indels 8; Gaps 1;

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OY 1281 gggtagaggtctgtgtcttacaccctgtatgtcttaacccttgagcttaaccct 1340
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 6 GAGTCTTCTCTGTGTGCCAGGCTGGAGTGCAGTGGCATGATCTGCTCACTGCACACT 65
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1341 ctgcctcccaaggttcaagaactctctgtctcaagcctcccgctagcttgagactaagg 1400
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Accession	Sequence	Position
Db	CCACCTCCCAATTCAAGGATTCTCTCCACGCTCCCAATGAGCGGATTACAG	125
Oy	1401 cg-----cagcccgcgcaattcttgatctgtatgtagagatgagggcttcacarat	1452
Db	126 TGCCCAACCAACACACCACTGATTTTGTATTGTTAGTAGAGATGGGTTTCACCATAT	185
Oy	1453 tagcccgagcttgctcttgaactctcgaactcgaagtatccaccacactcagctcctaag	1512
Db	186 TGCGCAGACTGGTCTTCGAACCTCTTCAACCTCAACGATGATCCACCGGCTCAGCTCCACAGAG	245
Oy	1513 tgcctggattcaagagcatgagtcacgcgcgcgcgcaagggctcagtgcttaataagaaat	1572
Db	246 TGCTGGGATATTATAGGCGTGAAGCCACCGCGCGCTTGCGACAGAGCTTTTAAAGAAAG	305
Oy	1573 aa 1574	
Db	306 aa 307	

RESULT	10
LOCUS	A0112451
DEFINITION	AA0112451 516 bp DNA GSS 29-AUG-1998
ACCESSION	CTT-HSP-2372C9.TF CTT-HSP Homo sapiens genomic clone 2372C9, DNA sequence.
VERSION	A0112451
KEYWORDS	A0112451.1 GI:3484611
SOURCE	GSS.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo. 1 (bases 1 to 516)
	Adams,M.D., Kounitsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., and berry,K., Ganger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other-GSS: CTT-HSP-2372C9.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 7112 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.

FEATURES	LOCATION/Qualifiers
SOURCE	1. .516
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="2372C9"
	/clone_1lb="CIT-HSP"
	/sex="Male"
	/cell_type="Sperm"
	/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT	87 a 145 c 118 g 166 t
ORIGIN	

Query Match	2.9%	Score 177.6;	DB 224;	Length 516;
Best Local Similarity	85.2%	Pred. No. 2.2e-21;		
Matches 213;	Conservative	0;	Mismatches 29;	Indels 8; Gaps 1
QY 1321	actctggacccacatgcgaacctctgcctccccaaggttaagaacaattctctgtcttaagccttc	1380		
Db 255	atttcagctcactgcgaacactctgcctcccggggttaaacgattctccctgcttcagccctcc	314		

[illegible]

RESULT	11				
LOCUS	A0265389/c				
DEFINITION	A0265389	577 bp	DNA	GSS	27-Oct-1998
ACCESSION	CITR1-El-2509010.TF		CITR1-El	Homo sapiens genomic clone 2509010,	
VERSION	A0265389			DNA sequence.	
KEYWORDS	A0265389.1	GI:3793589			
SOURCE	GSS.				
ORGANISM	human.				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo. 1 (bases 1 to 577) Adams,M.D., Rounsley,S.D., Zhao,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.				
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building				
JOURNAL	Unpublished (1998)				
COMMENT	Other:GSS: CITR1-El-2509010.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.				

FEATURES	SOURCE
location/Qualifiers	1. 577
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="2509010"	
/clone_lib="Cftr1-E1"	
/sex="male"	
/cell_type="sperm"	
/note="vector: pBeloBAC11, Site_1: EcoRI; Site_2: EcoRI; CalTech Human BAC Library D"	
BASE COUNT	167 a 127 c 137 g 146 t
ORIGIN	

Query Match	2.9%	Score 177.4	DB 226	length 577
Best Local Similarity	75.1%	Pred. NO	2.4e-21	
Matches 228	Conservative	0	Mismatches 71	Indels 8
			Gaps	1
QY	1321	acctgagctcaactgtcaacctctgctctccaggtttcaagaacattctctgtctcaagcttc	1380	
	1			
	1			
Db	368	attctcgcttactgcgaacctctgctctccaggtttcaagaacattctctgtctcaagcttc	309	
	1381	cgctgtactgtgagactcaagc-----gcagcgcgcgcgaacttttgtatttgtatga	1432	

Accession	Sequence	Position
Dh	CGAGATCTAGACTACGAGCACCCGCCAACCAACCTGGCAATTTTTCGATTTTAACTA	249
Qy	gagatggggttttcaacatlatagccggcctcgggtcttgaaactcttgacctgaagtgtatcca	1492
Dh	GAGACGGGGGTTTACCAATGTTGGTCAGAGCTGGTCTTAACCTCCGACCTCAGCGGATCCA	189
Qy	cccaacctcagcctctcaaaatgctcgggatactaaagca tgaatcaaccgycgcgcggccaag	1552
Dh	CCCCCTTGGGCTCCCAAGGCGGGGATTTACAGGCAATGAGCCACTCACCACGCCACGA	129
Qy	gtcagtgcttcaataaggaataaacttgaatggtttactcaaaacaaaggaagaaagacaaa	1612
Dh	GATACATTTTGTGAATATCTAGACCTGGAAGCTCAGTGCAGACACGCTCCGCAAGCAAGGAAT	69
Qy	agctcgtgataaattcag 1629	
Dh	AGTAATACTGGTATGAG 52	

RESULT 12	LOCUS	DEFINITION
AI583291/c	AI583291	548 bp mRNA EST 14-DEC-1999
		tt56g02.x1 NCI CGAP_HSC4 Homo sapiens cDNA clone IMAGE:2244818 3'
		similar to TR:Q13538 Q13538 ORF: FUNCTION UNKNOWN. ;contains Alu
		repetitive element; mRNA sequence.

ACCESSION	AI583291	
VERSION	AI583291.1	GI:4569188
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE Eukaryotic: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 548)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg Ph.D.

Contact: Robert Strausberg, Ph.D.
 Email: cgnabs-r@mail.nih.gov
 Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 cDNA Library Preparation: David B. Kitzman, Ph.D.
 cDNA library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution Information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/brp/IMAGE/IMAGE.html
 Insert Length: 664 Std Error: 0.00
 Seq primer: -40UP from Gldco
 High quality sequence stop: 464
 SOLYA-NO.

FEATURES	Location/Qualifiers
SOURCE	1. 548

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2244818"
/clone_id="NCI_CGAP_HSC4"
/tissue_type="CD34+", CD38- from normal bone marrow donor
/lab_host="DH108"
/note="Organ: bone marrow; Vector: PAMPI; mRNA made from
lymphoid tissue; cDNA made by oligo-dT priming.
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified. cDNA library preparation: David B.
Kritzman, Ph.D. Reference: Kritzman et al. (1996) Cancer
Research 56:5380-5383."

```

Query Match	2.98;	Score 177.2;	DB 22;	Length 548
Best Local Similarity	78.88;	Pred. No. 2.6e-21;		

Matches	227	Conservative	0	Mismatches	53	Indels	8	Gaps	1
QY	1277	gtgaggtgagaggtctctgtcttaacactactcgtatgctctaacacctgagcttaactgca							1336
Db	546	GAGGAGTCTTGATGTTGTCTCAGGCGTGGAGTGGACGTGGATGATCTTGGCTGACTGCA							487
QY	1337	aacctgcgtccccaagttcaagaacattccctcgtctcaagccctcccgctagcttgagacta							1396
Db	486	ACCTCGCGCTCAGACGTTCAAGCATTTCTCGCTCAGCCTCTCTGAGCAGCTGAGACTA							427
QY	1397	cagggg-----caagcccggtcgaattttgtatctgttagtaagaatggggtttcac							1448
Db	426	CAGGGCGCCCGCACACACGCTGGCTAAATTTTGTATTTTAACTAGAGATGGGGTTTCACC							367
QY	1449	atatattgacccggtgtgtcttgaacacctgagacctcaagtgatcatccacaactcaagctcct							1508
Db	366	ATGTGGGCGACAGCTGTGTGAACTCTGAACTCTGACCTCAGATGATCACACCACTTGGTCTCC							307
QY	1509	aaagtgcttggaattacaagcatgaatcaacggcgcccgagcaagggtca							1556
Db	306	AAAGTCTGTGGATTACAGGATGAGCCACCGCTGCCAGCCCAAGATTTA							259

RESULT	13
BF920612/c	
LOCUS	BF920612
DEFINITION	400 bp mRNA
ACCESSION	U00-NT0151-081100-455-f04 NT0151
VERSION	BF920612
KEYWORDS	BF920612.1 GI:12316500
SOURCE	EST.
	human.
	EST
	19-JAN-2001
	CDNA, mRNA sequence

ORGANISM	REFERENCE
Homo sapiens	
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi	
Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.	
1 (bases 1 to 400)	
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. B.	

TITLE	JOURNAL	MEDLINE	COMMENT
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags	Proc. Natl. Acad. Sci. U.S.A.	97 (7), 3491-3496 (2000)	
Simpson, A.J.			
Nagai, M.A., da Silva, W. Jr., Zagó, M.A., Bordin, S., Costa, F.P., Goldani, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			
Contact: Simpson A.J.G.			

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?LI=00652-QV0-NT0151>)
 081100-455-E046r3-2000-11-08a4t-1)
 Seq primer: puc 18 forward
 High quality sequence start: 4
 High quality sequence stop: 400.

FEATURES	Location/Qualifiers
source	1. .400

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="NT0151"
/notes="Organ: nervous tumor; Vector: puc18; Site: 1: SM1;
Site:2: SM1; A mini-library was made by cloning products
derived from ORSTS PCR (U.S. letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```



```

Db 192 CCACCTCCAGGTTCAAGCAATTCCTGTCACAGCTCCTAAGTAGCTGGGACTAGAAG 251
Oy 1401 cgcacg-----ccggcctaatttctgtatgtltagtagagatggggttccacatat 1452
Db 252 GGGCCGCCACCATACCAAGCTAATTTTCTATTATTAGTAGAGATGGGGTTTCACCATAT 311
Oy 1453 tagcccgctgtgtcttgacctcgaactcaagtgatccaccacctcagcctcctaaag 1512
Db 312 TGGTCAGGCTGCTTTGAATCTCTACCTCAGGTGATCCACCGCTTGCCCTCCCAAG 371
Oy 1513 tgcctgggattacagcatgagtcaccgcgcccgcgaaggtcagtglttaataaagaaat 1572
Db 372 TGCTGGATGACAGGCGTGAGCCACTGGCCGCCACCAAGTTCTGGAATTTTAAGCCAA 431
Oy 1573 aactggaatggttactaaaccaacagggaaaacagaaagctg 1617
Db 432 AATATTAATCTATTTAACACTCAATGGCATTTACTCACAGAGATG 476

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Search completed: November 8, 2001, 12:56:07
 Job time: 17207 sec

